

**SEQUENCE LISTING**

**(1) GENERAL INFORMATION**

(i) APPLICANT: Wong, Hing C.  
Jiao, Jin-an  
Esperanza, Nieves  
Lawrence, Luepschen

(ii) TITLE OF THE INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS OF USE THEREOF

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
- (B) STREET: 130 Water Street
- (C) CITY: Boston
- (D) STATE: MA
- (E) COUNTRY: USA
- (F) ZIP: 02109

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Corless, Peter F
- (B) REGISTRATION NUMBER: 33,860
- (C) REFERENCE/DOCKET NUMBER: 46943

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 617-523-3400
- (B) TELEFAX: 617-523-6440
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACATTAGA TGACCCAGTC TCCTGCCTCC CAGTCTGCAT CTCTGGGAGA AAGTGTCA	60
ATCACATGCC TGGCAAGTCA GACCATTGAT ACATGGTTAG CATGGTATCA GCAGAAACCA	120
GGGAAATCTC CTCAGCTCCT GATTATGCT GCCACCAACT TGGCAGATGG GGTCCCATCA	180
AGGTTCACTG GCAGTGGATC TGGCACAAAA TTTTCTTCA AGATCAGCAG CCTACAGGCT	240
GAAGATTTCG TAAATTATTA CTGTCAACAA GTTACAGTT CTCCATTAC GTCGGTGCT	300
GGGACCAAGC TGGAGCTGAA A	321

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE: N-terminal
  - (vi) ORIGINAL SOURCE:
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp	Ile	Gln	Met	Thr	Gin	Ser	Pro	Ala	Ser	Gln	Ser	Ala	Ser	Leu	Gly
1			5						10				15		
Glu	Ser	Val	Thr	Ile	Thr	Cys	Leu	Ala	Ser	Gln	Thr	Ile	Asp	Thr	Trp
				20					25				30		
Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ser	Pro	Gln	Leu	Leu	Ile
						35			40			45			
Tyr	Ala	Ala	Thr	Asn	Leu	Ala	Asp	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly
					50			55			60				
Ser	Gly	Ser	Gly	Thr	Lys	Phe	Ser	Phe	Lys	Ile	Ser	Ser	Leu	Gln	Ala
65				70					75				80		
Glu	Asp	Phe	Val	Asn	Tyr	Tyr	Cys	Gln	Gln	Val	Tyr	Ser	Ser	Pro	Phe
					85					90			95		
Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys					
					100				105						

**(2) INFORMATION FOR SEQ ID NO:3:**

- (i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 351 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA  
(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAGATCCAGC TGCAGCAGTC TGGAACCTGAG CTGGTGAAGC CTGGGGCTTC AGTGCAGGTA 60  
TCCTGCAAGA CTTCTGGTTA CTCATTCACT GACTACAACG TGTACTGGGT GAGGCAGAGC 120  
CATGGAAAGA GCCTTGAGTG GATTGGATAT ATTGATCCTT ACAATGGTAT TACTATCTAC 180  
GACCAGAACT TCAAGGGCAA GGCCACATTG ACTGTTGACA AGTCTTCCAC CACAGCCTTC 240  
ATGCATCTCA ACAGCCTGAC ATCTGACGAC TCTGCAGTTT ATTTCTGTGC AAGAGATGTG 300  
ACTACGGCCC TTGACTCTG GGGCCAAGGC ACCACTCTCA CAGTCTCCTC A 351

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala

1 5 10 15

Ser Val Gln Val Ser Cys Lys Thr Xaa Gly Tyr Ser Phe Thr Asp Tyr

20 25 30

Asn Val Tyr Trp Val Arg Gln Ser His Gly Lys Ser Leu Glu Trp Ile

35 40 45

Gly Tyr Ile Asp Pro Tyr Asn Gly Ile Thr Ile Tyr Asp Gln Asn Phe  
           50                  55                  60  
 Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Phe  
       65                  70                  75                  80  
 Met His Leu Asn Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys  
           85                  90                  95  
 Ala Arg Asp Val Thr Thr Ala Leu Asp Phe Trp Gly Gln Gly Thr Thr  
           100                 105                  110  
 Leu Thr Val Ser Ser  
                           ,  
           115

**(2) INFORMATION FOR SEQ ID NO:S:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

**(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:**

Leu Ala Ser Gln Thr Ile Asp

1                  5

**(2) INFORMATION FOR SEQ ID NO:6:**

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE: N-terminal
  - (vi) ORIGINAL SOURCE:
- 
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Ala Thr Asn Leu Ala Asp  
1                       5

**(2) INFORMATION FOR SEQ ID NO:7:**

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: N-terminal
- (vi) ORIGINAL SOURCE:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gln Gln Val Tyr Ser Ser Pro Phe Thr  
1                       5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr Asp Tyr Asn Val Tyr

1

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Tyr Ile Asp Pro Tyr Asn Gly Ile Thr Ile Tyr Asp Gln Asn Phe Lys  
1                   5                   10                   15  
Gly

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE: N-terminal

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Val Thr Thr Ala Leu Asp Phe

1                   5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGGCAAGTC AGACCATTGA T

21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCTGCCACCA ACTTGGCAGA T

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAACAAGTTT ACAGTTCTCC ATTCACGT 28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTGACTACA ACGTGTAC 18

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TATATTGATC CTTACAATGG TATTACTATC TACGACCAGA ACTTCAAGGG C 51

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GATGTGACTA CGGCCCTTGA CTTC

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCACCTCCAG ATGTTAACTG CTC

23

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAARTAVCCC TTGACCAGGC

20

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GGAGGCAGGCG GTTCTGACAT TGTGMTGWCM CARTC

35

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATTCAGGCC CAGCCGGCCA TGGCCGARGT YCARCTKCAR CARYC 45

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCCGGGCCAC CATGKCCCCW RCTCAGYTYC TKG

33

(2) INFORMATION FOR SEQ ID NO:22:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCCGGGCCAC CATGGRATGS AGCTGKGTMA TSCTC

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATATACTCGC GACAGCTACA GGTGTCCACT CCGAGATCCA  
GCTGCAGCAG TC

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GACCTGAATT CTAAGGAGAC TGTGAGAGTG G

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTAATTGATA TCCAGATGAC CCAGTCTCC

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 45 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TAATCGTCG AAAAGTGTAC TTACGTTCA GCTCCAGCTT GGTCC